

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

Claims 1-20 (Canceled)

21. (Currently Amended) A method for sequencing a heterogeneous population of single stranded DNA molecules simultaneously and without spatial resolution, wherein each DNA molecule is present in a unique amount and each DNA molecule bears a primer that provides a double stranded portion, which method comprises the following steps:

a) contacting the population of single stranded DNA molecules with an array of hybridization probes, each probe comprising a mass label cleavably attached to a known base sequence of predetermined length, the array containing all base sequences being incapable of ligation to each other, wherein the contacting is carried out in the presence of ligase under conditions to ligate to the double stranded portion of each DNA molecule to the probe bearing the base sequence complementary to the single stranded portion of each DNA molecule adjacent to the double stranded portion thereby to form an extended double stranded portion which is incapable of ligation to further probes; and

b) removing all unligated probes; followed by the steps of:

c) cleaving the mass label from the extended double stranded portion;

d) simultaneously recording quantity of each mass label using mass spectrometry;

e) activating the extended double stranded portion to enable ligation thereto; wherein

f) steps (a) to (e) are repeated in a cycle for a sufficient number of times to determine the sequence of each single stranded DNA molecule by determining the sequence of release of each label;

wherein the sequence of each DNA molecule is identified on the basis of the relative quantities of each mass label recorded in step (d) and the unique amount of each DNA molecule.

22. (Original) A method according to claim 21, wherein the array comprises a plurality of sub-arrays which together contain all the possible base sequences, and wherein each sub-array is contacted with the DNA population according to step (b), unligated probes are removed according to step (c), and these steps are repeated in a cycle before step (d) so that all of the subarrays contact the DNA population.

23. (Previously Presented) A method according to claim 21, wherein the heterogenous population of single stranded DNA molecules is obtained by sorting an initial DNA sample into sub-populations and selecting one of the subpopulations as the target DNA population.

24. (Original) A method according to claim 23, wherein the initial DNA sample is cut into fragments, each having a sticky end of known length and unknown sequence, which fragments are sorted into sub-populations according to their sticky end sequence.

25. (Original) A method according to claim 21, wherein each single-stranded DNA is immobilized at one end.

26. (Canceled)

27. (Original) A method according to claim 21, wherein the known base sequence is blocked at its 3'OH.

28. (Original) A method according to claim 27, wherein the step (d) of cleaving the ligated probes to release each label unblocks the 3'-OH of the extended double-stranded portion according to step (f).

29. (Original) A method according to claim 28, wherein the label of each probe is cleavably attached to the 3'-OH of the base sequence.

30. (Original) A method according to claim 21, wherein the base sequence of each probe is unphosphorylated at both 3' and 5' ends and step (f) comprises phosphorylating the 5'-OH of the extended double-stranded portion.

31. (Original) A method according to claim 21, wherein the predetermined length of the base sequence is from 2 to 6.

32. (Original) A method according to claim 31, wherein the predetermined length of the base sequence is 4.

Claims 33-43. (Canceled)